

SEQUENCE LISTING

<110> Kufer, et al.

<120> Heterominibodies

<130> 009848/027 6371

<140> 09/744,625

<141> 2001-07-16

<150> EP 98 11 4082.5

<151> 1998-07-28

<160> 39

<170> PatentIn Ver. 2.1

<210> 1

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no natural origin

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aattccggaa ccccgctggg tgacaccacc cacaccgta cgggtggctgc accatctgtc 60
ttc 63

<210> 2

<211> 46

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<223> Description of Artificial Sequence: synthetic, no natural origin

<400> 2

ataagaatgc ggccgcgtcg actaacactc tcccctgttg aagctc 46

<210> 3

<211> 33

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic, no natural origin

<400> 3

gcagaattca ccatgggcca cacacggagg cag 33

<210> 4

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 4

tggtccggag ttatcaggaa aatgctcttg cttg

34

<210> 5

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 5

aattccggaa ccccgctggg tgacaccacc cacaccgcta gcaccaaggg cccatcggtc 60
ttcc 64

<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 6

aattccggaa ctagttttgt cacaagattt gg

32

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 7

ctcgaattca ctatggctcc cagcagcccc cg

32

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 8

gattccggac' tcataccggg gggagagcac

30

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 9
aatctagaac catggttgct gggagcgacg 30

<210> 10
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 10
aagtcggat ctgtgtcttg aatgaccgct gc 32

<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 11
aagtctagaa aatggatccc cagtgcacta tg 32

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 12
aattccggat gggggaggct gagggctctc aagc 34

<210> 13
<211> 64
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 13
cctgagctcg cccgtcacaa agagcttcaa caggggagag tgtggaggtg gtggatccga 60
tatc 64

<210> 14
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 14
attctagagc ggccgcgctg actatttcag ctccagcttg gtcccagc 48

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 15
gtcacctct cctccggag 19

<210> 16
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 16
gtgtccgat ttcagctcca gcttggtcc 29

<210> 17
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 17
gtcacctct cctccggag 19

<210> 18

<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 18
ggtgtgggtg gtgtcacc

18

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 19
gcagaattca ccatgggcca cacacggagg cag

33

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 20
tgggccggag ttatcaggaa aatgctcttg cttg

34

<210> 21
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 21
aggtgtacac tccgatatcm arctgcagsa gtcwgg

36

A/C = M
A/G = R
G/C = S
A/T = W

<210> 22
<211> 64
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 22

ggagccgccc cgcgcagaac caccaccacc tgcggagacg gtgaccgtgg tcccttggcc 60
ccag 64

<210> 23

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 23

ggcggcggcg gctccggtgg tgggtggttct gacattcagc tgaccagtc tcca 54

<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 24

aatccggatt tgatctcgag cttggtccc 29

<210> 25

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 25

ctagaattct tcgaatccgg aggtggtgga tccgatatcc ccgggcatca tcaccatcat 60
cattgag 67

<210> 26

<211> 796

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (11)..(793)

<400> 26

gaattccacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca 49
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr
1 5 10

gct aca ggt gta cac tcc gat atc gtt gtg act cag gaa tct gca ctc	97
Ala Thr Gly Val His Ser Asp Ile Val Val Thr Gln Glu Ser Ala Leu	
15 20 25	
acc aca tca cct ggt gaa aca gtc aca ctc act tgt cgc tca agt act	145
Thr Thr Ser Pro Gly Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Thr	
30 35 40 45	
ggg gct gtt aca act agt aac tat gcc aac tgg gtc caa gaa aaa cca	193
Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro	
50 55 60	
gat cat tta ttc act ggt cta ata ggt ggt acc aac aac cga gtt cca	241
Asp His Leu Phe Thr Gly Leu Ile Gly Gly Thr Asn Asn Arg Val Pro	
65 70 75	
ggt gtt cct gcc aga ttc tca ggc tcc ctg att gga gac aag gct gcc	289
Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala	
80 85 90	
ctc acc atc aca ggg gca cag act gag gat gag gca ata tat ttc tgt	337
Leu Thr Ile Thr Gly Ala Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys	
95 100 105	
gct cta tgg tac agc aac cat tgg gtg ttc ggt gga gga acc aaa ctc	385
Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu	
110 115 120 125	
gag gtc cta ggt ggt ggt ggt tct ggc ggc ggc ggc tcc ggt ggt ggt	433
Glu Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly	
130 135 140	
ggt tct cag gtc cag ctg cag gag tct gga cct ggc ctg gtg gcg ccc	481
Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro	
145 150 155	
tca cag agc ctg tcc atc aca tgc acc atc tca ggg ttc tca tta act	529
Ser Gln Ser Leu Ser Ile Thr Cys Thr Ile Ser Gly Phe Ser Leu Thr	
160 165 170	
aag tat ggt gta cac tgg gtt cgc cag cct cca gga aag ggt ctg gag	577
Lys Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu	
175 180 185	
tgg ctg gtg gtg ata tgg act gat gga ggc aca tcc tat aat tca gct	625
Trp Leu Val Val Ile Trp Thr Asp Gly Gly Thr Ser Tyr Asn Ser Ala	
190 195 200 205	
ctc aaa tcc aga ctg agc atc agc aag gac aac tcc aag agc caa gtt	673
Leu Lys Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val	
210 215 220	
ttc tta aaa atg aac agt ctc caa act gat gac aca gcc atg tac tac	721
Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr	
225 230 235	
tgt gcc aga cag gat aga tac gac ggt gga att gct tac tgg ggc caa	769
Cys Ala Arg Gln Asp Arg Tyr Asp Gly Gly Ile Ala Tyr Trp Gly Gln	
240 245 250	

ggg acc acg gtc acc gtc tcc tcc gga
 Gly Thr Thr Val Thr Val Ser Ser
 255 260

796

<210> 27
 <211> 261
 <212> PRT
 <213> Mus musculus

<400> 27
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser Asp Ile Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser
 20 25 30
 Pro Gly Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val
 35 40 45
 Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu
 50 55 60
 Phe Thr Gly Leu Ile Gly Gly Thr Asn Asn Arg Val Pro Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile
 85 90 95
 Thr Gly Ala Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp
 100 105 110
 Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Glu Val Leu
 115 120 125
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 130 135 140
 Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
 145 150 155 160
 Leu Ser Ile Thr Cys Thr Ile Ser Gly Phe Ser Leu Thr Lys Tyr Gly
 165 170 175
 Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val
 180 185 190
 Val Ile Trp Thr Asp Gly Gly Thr Ser Tyr Asn Ser Ala Leu Lys Ser
 195 200 205
 Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
 210 215 220
 Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 225 230 235 240
 Gln Asp Arg Tyr Asp Gly Gly Ile Ala Tyr Trp Gly Gln Gly Thr Thr
 245 250 255
 Val Thr Val Ser Ser
 260

<210> 28
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 28
ccggaggtgg tggttccggg ggtggagggt caggcgggtg tg 42

<210> 29
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic, no
natural origin

<400> 29
gatccaccac cgcctgaacc tccacccccg gaaccaccac ct 42

<210> 30
<211> 1371
<212> DNA
<213> Homo sapiens/Mus musculus

<220>
<221> CDS
<222> (10)..(1359)

<400> 30
gaattcacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct 51
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala
1 5 10

aca ggt gta cac tcc gat atc cag ctg acc cag tct caa aaa ttc atg 99
Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Gln Lys Phe Met
15 20 25 30

tcc aca tca gta gga gac agg gtc agc gtc acc tgc aag gcc agt cag 147
Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln
35 40 45

aat gtg ggt act aat gta gcc tgg tat caa cag aaa cca ggg caa tct 195
Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
50 55 60

cct aaa gca ctg att tac tgc gca tcc tac cgg tac agt gga gtc cct 243
Pro Lys Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro
65 70 75

gat cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc atc 291
Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

80	85	90	
agc aat gtg cag tct gaa gac ttg gca gag tat ttc tgt cag caa tat			339
Ser Asn Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr			
95 100 105 110			
aac agc tat ccg ctc acg ttc ggt gct ggg acc aag ctc gag atc aaa			387
Asn Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys			
115 120 125			
ggt ggt ggt ggt tct ggc ggc ggc ggc tcc ggt ggt ggt ggt tct cag			435
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln			
130 135 140			
gtg aaa ctg cag gag tca gga cct ggc cta gtg cag ccc tca cag agc			483
Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser			
145 150 155			
ctg tcc atc acc tgc aca gtc tct ggt ttc tca tta act agc tat ggt			531
Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly			
160 165 170			
gta cac tgg gtt cgc cag tct cca gga aag ggt ctg gag tgg ctg gga			579
Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly			
175 180 185 190			
gtg ata tgg agt ggt gga agc aca gac tat aat gca gct ttc ata tcc			627
Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser			
195 200 205			
aga ctg agc atc agc aag gac aat tcc aag agc caa gtt ttc ttt aaa			675
Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys			
210 215 220			
atg aac agt ctg caa gct aat gac aca gcc ata tat tac tgt gcc aga			723
Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala Arg			
225 230 235			
atg gag aac tgg tgc ttt gct tac tgg ggc caa ggg acc acg gtc acc			771
Met Glu Asn Trp Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr			
240 245 250			
gtc tcc gaa ttc ccc aaa cct agc acc ccc cct ggc agc agt ggt gaa			819
Val Ser Glu Phe Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly Glu			
255 260 265 270			
ctg gaa gag ctg ctt aag cat ctt aaa gaa ctt ctg aag ggc ccc cgc			867
Leu Glu Glu Leu Leu Lys His Leu Lys Glu Leu Leu Lys Gly Pro Arg			
275 280 285			
aaa ggc gaa ctc gag gaa ctg ctg aaa cat ctg aag gag ctg ctt aaa			915
Lys Gly Glu Leu Glu Glu Leu Leu Lys His Leu Lys Glu Leu Leu Lys			
290 295 300			
ggt ggg agc gga ggc gcg ccg gca cct act tca agt tct aca aag aaa			963
Gly Gly Ser Gly Gly Ala Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys			
305 310 315			
aca cag cta caa ctg gag cat tta ctg ctg gat tta cag atg att ttg			1011
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu			
320 325 330			

aat gga att aat aat tac aag aat ccc aaa ctc acc agg atg ctc aca	1059
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr	
335 340 345 350	

ttt aag ttt tac atg ccc aag aag gcc aca gaa ctg aaa cat ctt cag	1107
Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln	
355 360 365	

tgt cta gaa gaa gaa ctc aaa cct ctg gag gaa gtg cta aat tta gct	1155
Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala	
370 375 380	

caa agc aaa aac ttt cac tta aga ccc agg gac tta atc agc aat atc	1203
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile	
385 390 395	

aac gta ata gtt ctg gaa cta aag gga tct gaa aca aca ttc atg tgt	1251
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys	
400 405 410	

gaa tat gct gat gag aca gca acc att gta gaa ttt ctg aac aga tgg	1299
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp	
415 420 425 430	

att acc ttt tgt caa agc atc atc tca aca ctg act gac gtc cat cac	1347
Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Asp Val His His	
435 440 445	

cat cac cat cac tgataagtcg ac	1371
His His His His	
450	

<210> 31

<211> 450

<212> PRT

<213> Homo sapiens/Mus musculus

<400> 31

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Gln Leu Thr Gln Ser Gln Lys Phe Met Ser Thr
20 25 30

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val
35 40 45

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
50 55 60

Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg
65 70 75 80

Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn
85 90 95

Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser
100 105 110

Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Gly Gly
 115 120 125
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Lys
 130 135 140
 Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser
 145 150 155 160
 Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly Val His
 165 170 175
 Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile
 180 185 190
 Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu
 195 200 205
 Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn
 210 215 220
 Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Met Glu
 225 230 235 240
 Asn Trp Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 245 250 255
 Glu Phe Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly Glu Leu Glu
 260 265 270
 Glu Leu Leu Lys His Leu Lys Glu Leu Leu Lys Gly Pro Arg Lys Gly
 275 280 285
 Glu Leu Glu Glu Leu Leu Lys His Leu Lys Glu Leu Leu Lys Gly Gly
 290 295 300
 Ser Gly Gly Ala Pro Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
 305 310 315 320
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
 325 330 335
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 340 345 350
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
 355 360 365
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
 370 375 380
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
 385 390 395 400
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 405 410 415
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 420 425 430
 Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Asp Val His His His His

435

440

445

His His
450

<210> 32

<211> 1389

<212> DNA

<213> Homo sapiens/Mus musculus

<220>

<221> CDS

<222> (10) .. (1377)

<400> 32

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala
1 5 10

aca ggt gta cac tcc gat atc cag ctg acc cag tct caa aaa ttc atg 99
Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Gln Lys Phe Met
15 20 25 30

tcc aca tca gta gga gac agg gtc agc gtc acc tgc aag gcc agt cag 147
Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln
35 40 45

aat gtg ggt act aat gta gcc tgg tat caa cag aaa cca ggg caa tct 195
Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
50 55 60

cct aaa gca ctg att tac tcg gca tcc tac cgg tac agt gga gtc cct 243
Pro Lys Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro
65 70 75

gat cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc atc 291
Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
80 85 90

agc aat gtg cag tct gaa gac ttg gca gag tat ttc tgt cag caa tat 339
Ser Asn Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr
95 100 105 110

aac agc tat ccg ctc acg ttc ggt gct ggg acc aag ctc gag atc aaa 387
Asn Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
115 120 125

ggt ggt ggt ggt tct ggc ggc ggc ggc tcc ggt ggt ggt ggt tct cag 435
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

gtg aaa ctg cag gag tca gga cct ggc cta gtg cag ccc tca cag agc 483
Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
145 150 155

ctg tcc atc acc tgc aca gtc tct ggt ttc tca tta act agc tat ggt 531
Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly
160 165 170

gta	cac	tgg	gtt	cgc	cag	tct	cca	gga	aag	ggc	ctg	gag	tgg	ctg	gga	579
Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	
175				180						185					190	
gtg	ata	tgg	agt	ggc	gga	agc	aca	gac	tat	aat	gca	gct	ttc	ata	tcc	627
Val	Ile	Trp	Ser	Gly	Gly	Ser	Thr	Asp	Tyr	Asn	Ala	Ala	Phe	Ile	Ser	
				195					200					205		
aga	ctg	agc	atc	agc	aag	gac	aat	tcc	aag	agc	caa	gtt	ttc	ttt	aaa	675
Arg	Leu	Ser	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Phe	Lys	
			210					215					220			
atg	aac	agt	ctg	caa	gct	aat	gac	aca	gcc	ata	tat	tac	tgt	gcc	aga	723
Met	Asn	Ser	Leu	Gln	Ala	Asn	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Arg	
		225					230					235				
atg	gag	aac	tgg	tgc	ttt	gct	tac	tgg	ggc	caa	ggg	acc	acg	gtc	acc	771
Met	Glu	Asn	Trp	Ser	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	
	240					245					250					
gtc	tcc	gaa	ttc	acc	ccg	ctg	ggc	gac	acc	acc	cac	acc	tcc	gga	aaa	819
Val	Ser	Glu	Phe	Thr	Pro	Leu	Gly	Asp	Thr	Thr	His	Thr	Ser	Gly	Lys	
255					260					265					270	
cca	ctg	gat	gga	gaa	tat	ttc	acc	ctt	cag	atc	cgt	ggg	cgt	gag	cgc	867
Pro	Leu	Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Gln	Ile	Arg	Gly	Arg	Glu	Arg	
				275					280					285		
ttc	gag	atg	ttc	cga	gag	ctg	aat	gag	gcc	ttg	gaa	ctc	aag	gat	gcc	915
Phe	Glu	Met	Phe	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp	Ala	
			290					295					300			
cag	gct	ggg	aag	gag	cca	ggg	ggg	agc	gga	ggc	gcg	ccg	gca	cct	act	963
Gln	Ala	Gly	Lys	Glu	Pro	Gly	Gly	Ser	Gly	Gly	Ala	Pro	Ala	Pro	Thr	
		305					310					315				
tca	agt	tct	aca	aag	aaa	aca	cag	cta	caa	ctg	gag	cat	tta	ctg	ctg	1011
Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	
	320					325					330					
gat	tta	cag	atg	att	ttg	aat	gga	att	aat	aat	tac	aag	aat	ccc	aaa	1059
Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	
335					340					345					350	
ctc	acc	agg	atg	ctc	aca	ttt	aag	ttt	tac	atg	ccc	aag	aag	gcc	aca	1107
Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	
				355					360					365		
gaa	ctg	aaa	cat	ctt	cag	tgt	cta	gaa	gaa	gaa	ctc	aaa	cct	ctg	gag	1155
Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	
			370					375					380			
gaa	gtg	cta	aat	tta	gct	caa	agc	aaa	aac	ttt	cac	tta	aga	ccc	agg	1203
Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	
		385					390					395				
gac	tta	atc	agc	aat	atc	aac	gta	ata	gtt	ctg	gaa	cta	aag	gga	tct	1251
Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	
	400					405					410					
gaa	aca	aca	ttc	atg	tgt	gaa	tat	gct	gat	gag	aca	gca	acc	att	gta	1299

Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val
415 420 425 430

gaa ttt ctg aac aga tgg att acc ttt tgt caa agc atc atc tca aca 1347
Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr
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Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
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Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg
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Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn
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Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser
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Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Lys
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Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser
145 150 155 160

Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly Val His
165 170 175

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile
180 185 190

Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu
195 200 205

Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn
210 215 220

Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Met Glu

225		230		235		240
Asn Trp Ser Phe	Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser					
	245		250		255	
Glu Phe Thr Pro	Leu Gly Asp Thr Thr His Thr Ser Gly Lys Pro Leu					
	260		265		270	
Asp Gly Glu Tyr	Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe Glu					
	275		280		285	
Met Phe Arg Glu	Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala					
	290		295		300	
Gly Lys Glu Pro	Gly Gly Ser Gly Gly Ala Pro Ala Pro Thr Ser Ser					
305		310		315		320
Ser Thr Lys Lys	Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu					
	325		330		335	
Gln Met Ile Leu	Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr					
	340		345		350	
Arg Met Leu Thr	Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu					
	355		360		365	
Lys His Leu Gln	Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val					
	370		375		380	
Leu Asn Leu Ala	Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu					
385		390		395		400
Ile Ser Asn Ile	Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr					
	405		410		415	
Thr Phe Met Cys	Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe					
	420		425		430	
Leu Asn Arg Trp	Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr					
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Asp Val His His	His His His His					
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aca ggt gta cac tcc gat atc cag ctg acc cag tct cca gca atc atg 99

Thr 15	Gly	Val	His	Ser	Asp 20	Ile	Gln	Leu	Thr	Gln 25	Ser	Pro	Ala	Ile	Met 30	
tct Ser	gca Ala	tct Ser	cca Pro	ggg Gly 35	gaa Glu	aag Lys	gtc Val	acc Thr 40	atg Met	acc Thr	tgc Cys	agg Arg	gcc Ala	agc Ser 45	tca Ser	147
agt Ser	gtt Val	agt Ser	tcc Ser 50	agt Ser	tac Tyr	ttg Leu	cac His	tgg Trp 55	tac Tyr	cag Gln	cag Gln	aag Lys	tca Ser 60	ggg Gly	gcc Ala	195
tcc Ser	ccc Pro	aaa Lys 65	ctc Leu	tgg Trp	att Ile	tat Tyr	agc Ser 70	aca Thr	tcc Ser	aac Asn	ttg Leu	gct Ala 75	tct Ser	gga Gly	gtc Val	243
cct Pro	gct Ala 80	cgc Arg	ttc Phe	agt Ser	ggc Gly	agt Ser 85	ggg Gly	tct Ser	ggg Gly	acc Thr 90	tct Ser	tac Tyr	tct Ser	ctc Leu	aca Thr	291
atc Ile 95	agc Ser	agt Ser	gtg Val	gag Glu	gct Ala 100	gaa Glu	gat Asp	gct Ala	gcc Ala	act Thr 105	tat Tyr	tac Tyr	tgc Cys	cag Gln 110	cag Gln	339
tac Tyr	agt Ser	ggg Gly	tac Tyr	ccg Pro 115	tac Tyr	acg Thr	ttc Phe	gga Gly	ggg Gly 120	ggg Gly	acc Thr	aag Lys	ctc Leu	gag Glu 125	atc Ile	387
aaa Lys	ggg Gly	ggg Gly	ggg Gly 130	ggg Gly	tct Ser	ggc Gly	ggc Gly	ggc Gly 135	ggc Gly	tcc Ser	ggg Gly	ggg Gly	ggg Gly 140	ggg Gly	tct Ser	435
cag Gln	gtg Val	aaa Lys 145	ctg Leu	cag Gln	gag Glu	tct Ser	ggg Gly 150	gct Ala	gag Glu	ctt Leu	gtg Val	aag Lys 155	cct Pro	ggg Gly	gct Ala	483
tca Ser	gtg Val 160	aag Lys	ctg Leu	tcc Ser	tgc Cys	aag Lys 165	gct Ala	tct Ser	ggc Gly	tac Tyr	acc Thr 170	ctc Leu	acc Thr	agc Ser	tac Tyr	531
tgg Trp 175	ttg Leu	cac His	tgg Trp	gtg Val	aag Lys 180	cag Gln	tgg Trp	cct Pro	gga Gly	cga Arg 185	ggc Gly	ctt Leu	gag Glu	tgg Trp 190	att Ile	579
gga Gly	agg Arg	att Ile	gat Asp	ccc Pro 195	aat Asn	agt Ser	ggg Gly	ggg Gly 200	act Thr	aag Lys	tac Tyr	gat Asp	gag Glu	aag Lys 205	ttc Phe	627
aag Lys	agc Ser	aag Lys	gcc Ala 210	aca Thr	ctg Leu	act Thr	gta Val	gac Asp 215	aaa Lys	ccc Pro	tcc Ser	agc Ser	aca Thr 220	gcc Ala	tac Tyr	675
atg Met	cag Gln	ctc Leu 225	agc Ser	agc Ser	ctg Leu	aca Thr	tct Ser 230	gag Glu	gac Asp	tct Ser	gcg Ala	gtc Val 235	tat Tyr	tat Tyr	tgt Cys	723
gca Ala 240	aga Arg	tgg Trp	gac Asp	tac Tyr	tgg Trp	ggc Gly 245	caa Gln	ggg Gly	acc Thr	acg Thr	gtc Val 250	acc Thr	gtc Val	tcc Ser	tcc Ser	771
gga Gly	acc Thr	ccg Pro	ctg Leu	ggg Gly	gac Asp	acc Thr	acc Thr	cac His	act Thr	agt Ser	gga Gly	aaa Lys	cca Pro	ctg Leu	gat Asp	819

255	260	265	270	
gga gaa tat ttc acc ctt cag atc cgt ggg cgt gag cgc ttc gag atg				867
Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe Glu Met	275	280	285	
ttc cga gag ctg aat gag gcc ttg gaa ctc aag gat gcc cag gct ggg				915
Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala Gly	290	295	300	
aag gag cca ggg ggg tcc gga ggt ggt ggt agc acc caa gtg tgc acc				963
Lys Glu Pro Gly Gly Ser Gly Gly Gly Gly Ser Thr Gln Val Cys Thr	305	310	315	
ggc aca gac atg aag ctg cgg ctc cct gcc agt ccc gag acc cac ctg				1011
Gly Thr Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu	320	325	330	
gac atg ctc cgc cac ctc tac cag ggc tgc cag gtg gtg cag gga aac				1059
Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn	335	340	345	350
ctg gaa ctc acc tac ctg ccc acc aat gcc agc ctg tcc ttc ctg cag				1107
Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln	355	360	365	
gat atc cag gag gtg cag ggc tac gtg ctc atc gct cac aac caa gtg				1155
Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val	370	375	380	
agg cag gtc cca ctg cag agg ctg cgg att gtg cga ggc acc cag ctc				1203
Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu	385	390	395	
ttt gag gac aac tat gcc ctg gcc gtg cta gac aat gga gac ccg ctg				1251
Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu	400	405	410	
aac aat acc acc cct gtc aca ggg gcc tcc cca gga ggc ctg cgg gag				1299
Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu	415	420	425	430
ctg cag ctt cga agc ctc aca gag atc ttg aaa gga ggg gtc ttg atc				1347
Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile	435	440	445	
cag cgg aac ccc cag ctc tgc tac cag gac acg att ttg tgg aag gac				1395
Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp	450	455	460	
atc ttc cac aag aac aac cag ctg gct ctc aca ctg ata gac acc aac				1443
Ile Phe His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn	465	470	475	
cgc tct cgg gcc tgc cac ccc tgt tct ccg atg tgt aag ggc tcc cgc				1491
Arg Ser Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg	480	485	490	
tgc tgg gga gag agt tct gag gat tgt cag agc ctg acg cgc act gtc				1539
Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val	495	500	505	510

tgt gcc ggt ggc	tgt gcc cgc tgc aag ggg cca ctg ccc act gac tgc	1587
Cys Ala Gly Gly	Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys	
515	520 525	
tgc cat gag cag	tgt gct gcc ggc tgc acg ggc ccc aag cac tct gac	1635
Cys His Glu Gln	Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp	
530	535 540	
tgc ctg gcc tgc ctc cac ttc aac cac agt ggc atc tgt gag ctg cac	1683	
Cys Leu Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His		
545	550 555	
tgc cca gcc ctg gtc acc tac aac aca gac acg ttt gag tcc atg ccc	1731	
Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro		
560	565 570	
aat ccc gag ggc cgg tat aca ttc ggc gcc agc tgt gtg act gcc tgt	1779	
Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys		
575	580 585 590	
ccc tac aac tac ctt tct acg gac gtg gga tcc tgc acc ctc gtc tgc	1827	
Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys		
595	600 605	
ccc ctg cac aac caa gag gtg aca gca gag gat gga aca cag cgg tgt	1875	
Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys		
610	615 620	
gag aag tgc agc aag ccc tgt gcc cga gtg tgc tat ggt ctg ggc atg	1923	
Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met		
625	630 635	
gag cac ttg cga gag gtg agg gca gtt acc agt gcc aat atc cag gag	1971	
Glu His Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu		
640	645 650	
ttt gct ggc tgc aag aag atc ttt ggg agc ctg gca ttt ctg ccg gag	2019	
Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu		
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agc ttt gat ggg gac cca gcc tcc aac act gcc ccg ctc cag cca gag	2067	
Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu		
675	680 685	
cag ctc caa gtg ttt gag act ctg gaa gag atc aca ggt tac cta tac	2115	
Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr		
690	695 700	
atc tca gca tgg ccg gac agc ctg cct gac ctc agc gtc ttc cag aac	2163	
Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn		
705	710 715	
ctg caa gta atc cgg gga cga att ctg cac aat ggc gcc tac tcg ctg	2211	
Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu		
720	725 730	
acc ctg caa ggg ctg ggc atc agc tgg ctg ggg ctg cgc tca ctg agg	2259	
Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg		
735	740 745 750	

gaa ctg ggc agt gga ctg gcc ctc atc cac cat aac acc cac ctc tgc	2307
Glu Leu Gly Ser Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys	
755 760 765	
ttc gtg cac acg gtg ccc tgg gac cag ctc ttt cgg aac ccg cac caa	2355
Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln	
770 775 780	
gct ctg ctc cac act gcc aac cgg cca gag gac gag tgt gtg ggc gag	2403
Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu	
785 790 795	
ggc ctg gcc tgc cac cag ctg tgc gcc cga ggg cac tgc tgg ggt cca	2451
Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro	
800 805 810	
ggg ccc acc cag tgt gtc aac tgc agc cag ttc ctt cgg ggc cag gag	2499
Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu	
815 820 825 830	
tgc gtg gag gaa tgc cga gta ctg cag ggg ctc ccc agg gag tat gtg	2547
Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val	
835 840 845	
aat gcc agg cac tgt ttg ccg tgc cac cct gag tgt cag ccc cag aat	2595
Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn	
850 855 860	
ggc tca gtg acc tgt ttt gga ccg gag gct gac cag tgt gtg gcc tgt	2643
Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys	
865 870 875	
gcc cac tat aag gac cct ccc ttc tgc gtg gcc cgc tgc ccc agc ggt	2691
Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly	
880 885 890	
gtg aaa cct gac ctc tcc tac atg ccc atc tgg aag ttt cca gat gag	2739
Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu	
895 900 905 910	
gag ggc gca tgc cag cct tgc ccc atc aac tgc acc cac tcc tgt gtg	2787
Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val	
915 920 925	
gac ctg gat gac aag ggc tgc ccc gcc gag cag aga gcc agc cct ctg	2835
Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu	
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Thr Ser Gly His His His His His His	
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Ser	Ser	Ser	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Ala	Ser	Pro		
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Lys	Leu	Trp	Ile	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala		
65					70					75					80		
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser		
				85					90					95			
Ser	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser		
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Gly	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly		
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Lys	Leu	Gln	Glu	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	Val		
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His	Trp	Val	Lys	Gln	Trp	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Ile	Gly	Arg		
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Ile	Asp	Pro	Asn	Ser	Gly	Gly	Thr	Lys	Tyr	Asp	Glu	Lys	Phe	Lys	Ser		
		195					200					205					
Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Pro	Ser	Ser	Thr	Ala	Tyr	Met	Gln		
	210					215					220						
Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg		
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Trp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Thr		
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Tyr	Phe	Thr	Leu	Gln	Ile	Arg	Gly	Arg	Glu	Arg	Phe	Glu	Met	Phe	Arg		
		275					280					285					
Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp	Ala	Gln	Ala	Gly	Lys	Glu		
	290					295					300						
Pro	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr		
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Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met		
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 340 345 350
 Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
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 Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
 370 375 380
 Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
 385 390 395 400
 Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
 405 410 415
 Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
 420 425 430
 Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
 435 440 445
 Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
 450 455 460
 His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser
 465 470 475 480
 Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp
 485 490 495
 Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala
 500 505 510
 Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His
 515 520 525
 Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu
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 Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro
 545 550 555 560
 Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
 565 570 575
 Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr
 580 585 590
 Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu
 595 600 605
 His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys
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 Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His
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 Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala
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 Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe

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	675						680					685			
Gln	Val	Phe	Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser
	690					695					700				
Ala	Trp	Pro	Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln
705					710					715					720
Val	Ile	Arg	Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu
				725					730					735	
Gln	Gly	Leu	Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu
			740					745					750		
Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val
		755					760					765			
His	Thr	Val	Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu
		770				775					780				
Leu	His	Thr	Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu
785					790					795					800
Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro
				805					810					815	
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			820					825					830		
Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala
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Val	Thr	Cys	Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His
865					870					875					880
Tyr	Lys	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys
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Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly
			900					905					910		
Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu
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<222> (39)..(1607)

<400> 36

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Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val His Ser Glu Leu Gln
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atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc 152
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
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acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat tgg 200
Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
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tat cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg gca 248
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
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tct acc cgg gaa tcc ggg gtc cct gac cga ttc agc ggc agt gaa tct 296
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Glu Ser
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ggg aca aat tac act ctc acc atc agc agc ctg cag cct gaa gat ttt 344
Gly Thr Asn Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
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gct act tac ttt tgt caa cag tct gac agt ttg ccg atc acc ttc ggc 392
Ala Thr Tyr Phe Cys Gln Gln Ser Asp Ser Leu Pro Ile Thr Phe Gly
          105          110          115

caa ggg aca cga ctg gac att caa gga gga gga gga tca ggt ggt ggt 440
Gln Gly Thr Arg Leu Asp Ile Gln Gly Gly Gly Gly Ser Gly Gly Gly
          120          125          130

ggt agc ggc ggc ggc ggc tca gag gtg cag ctg ctc gag tct ggg gga 488
Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
          135          140          145          150

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Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
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gga ttc acc ttc agt agc tat ggc atg cac tgg gtc cgc cag gct cca 584
Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro
          170          175          180

ggc aag ggg ctg gag tgg gtg gca gtt ata tca tat gat gga agt aat 632
Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn
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Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
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tgg aga ccc tac tac tac tac ggt atg gac gtc tgg ggc caa ggg acc Trp Arg Pro Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr 250 255 260			824
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agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr 295 300 305 310			968
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ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser 330 335 340			1064
ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr 345 350 355			1112
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gca ccc gcc cgc tcg ccc agc ccc agc acg cag ccc tgg gag cat gtg Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val 395 400 405			1256
aat gcc atc cag gag gcc cgg cgt ctc ctg aac ctg agt aga gac act Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr 410 415 420			1304
gct gct gag atg aat gaa aca gta gaa gtc atc tca gaa atg ttt gac Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp 425 430 435			1352
ctc cag gag ccg acc tgc cta cag acc cgc ctg gag ctg tac aag cag Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln 440 445 450			1400

ggc ctg cgg ggc agc ctc acc aag ctc aag ggc ccc ttg acc atg atg	1448
Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met	
455 460 465 470	
gcc agc cac tac aag cag cac tgc cct cca acc ccg gaa act tcc tgt	1496
Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys	
475 480 485	
gca acc cag att atc acc ttt gaa agt ttc aaa gag aac ctg aag gac	1544
Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp	
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Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu His	
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Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys	
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Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg	
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Phe Ser Gly Ser Glu Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser Ser	
85 90 95	
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Asp Ser	
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Leu Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Gln Gly Gly	
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Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln	
130 135 140	
Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg	
145 150 155 160	
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His	
165 170 175	

Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile		
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Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met		
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225					230					235					240		
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Gly	Asp	Thr	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro		
	275						280					285					
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly		
	290					295					300						
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Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser		
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Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser		
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	370					375					380						
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Gln	Pro	Trp	Glu	His	Val	Asn	Ala	Ile	Gln	Glu	Ala	Arg	Arg	Leu	Leu		
				405					410					415			
Asn	Leu	Ser	Arg	Asp	Thr	Ala	Ala	Glu	Met	Asn	Glu	Thr	Val	Glu	Val		
			420					425					430				
Ile	Ser	Glu	Met	Phe	Asp	Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg		
	435						440					445					
Leu	Glu	Leu	Tyr	Lys	Gln	Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys		
	450					455					460						
Gly	Pro	Leu	Thr	Met	Met	Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro		
465					470					475					480		
Thr	Pro	Glu	Thr	Ser	Cys	Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe		
				485					490					495			
Lys	Glu	Asn	Leu	Lys	Asp	Phe	Leu	Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp		

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505

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<212> DNA

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<222> (39)..(1610)

<400> 38

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Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val His Ser Glu Leu Gln
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atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc 152
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
25 30 35

acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat tgg 200
Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
40 45 50

tat cag cag aaa cca gga cag cct cct aag ctg ctc att tac tgg gca 248
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
55 60 65 70

tct acc cgg gaa tcc ggg gtc cct gac cga ttc agc ggc agt gaa tct 296
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Glu Ser
75 80 85

ggg aca aat tac act ctc acc atc agc agc ctg cag cct gaa gat ttt 344
Gly Thr Asn Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
90 95 100

gct act tac ttt tgt caa cag tct gac agt ttg ccg atc acc ttc ggc 392
Ala Thr Tyr Phe Cys Gln Gln Ser Asp Ser Leu Pro Ile Thr Phe Gly
105 110 115

caa ggg aca cga ctg gac att caa gga gga gga gga tca ggt ggt ggt 440
Gln Gly Thr Arg Leu Asp Ile Gln Gly Gly Gly Gly Ser Gly Gly Gly
120 125 130

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Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
135 140 145 150

ggc gtg gtc cag cct ggg agg tcc ctg aga ctc tcc tgt gca gcc tct 536
Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
155 160 165

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Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro	
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Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn	
185 190 195	
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Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp	
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Asp Thr Ala Val Tyr Cys Ala Lys Asp Met Gly Trp Gly Ser Gly	
235 240 245	
tgg aga ccc tac tac tac tac ggt atg gac gtc tgg ggc caa ggg acc	824
Trp Arg Pro Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr	
250 255 260	
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Thr Val Thr Val Ser Ser Gly Thr Pro Leu Gly Asp Thr Thr His Thr	
265 270 275	
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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu	
280 285 290	
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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe	
295 300 305 310	
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315 320 325	
tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc	1064
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser	
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acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag	1112
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu	
345 350 355	
aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg	1160
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser	
360 365 370	
ccc gtc aca aag agc ttc aac agg gga gag tgt tca gga ggc ggt ggg	1208
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser Gly Gly Gly Gly	
375 380 385 390	
tct gca cct act tca agt tct aca aag aaa aca cag cta caa ctg gag	1256
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu	
395 400 405	
cat tta ctg ctg gat tta cag atg att ttg aat gga att aat aat tac	1304

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
 410 415 420
 aag aat ccc aaa ctc acc agg atg ctc aca ttt aag ttt tac atg ccc 1352
 Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
 425 430 435
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 Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
 440 445 450
 aaa cct ctg gag gaa gtg cta aat tta gct caa agc aaa aac ttt cac 1448
 Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
 455 460 465 470
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 475 480 485
 cta aag gga tct gaa aca aca ttc atg tgt gaa tat gct gat gag aca 1544
 Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
 490 495 500
 gca acc att gta gaa ttt ctg aac aga tgg att acc ttt tgt caa agc 1592
 Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
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 atc atc tca aca cta act tgataagtcg acttaaaaca 1630
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<210> 39
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 <212> PRT
 <213> Homo sapiens/Mus musculus

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 Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys
 50 55 60
 Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg
 65 70 75 80
 Phe Ser Gly Ser Glu Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser Ser
 85 90 95
 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Asp Ser
 100 105 110
 Leu Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Gln Gly Gly
 115 120 125

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Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile		
			180					185						190			
Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg		
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Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met		
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				245					250					255			
Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Thr	Pro	Leu		
			260					265					270				
Gly	Asp	Thr	Thr	His	Thr	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile		
	275						280					285					
Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val		
	290					295					300						
Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys		
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Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu		
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		355					360					365					
His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu		
	370					375					380						
Cys	Ser	Gly	Gly	Gly	Gly	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys		
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			420					425					430				
Phe	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln		
		435					440					445					

Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala
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Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile
465					470					475					480
Asn	Val	Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys
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			500					505					510		
Ile	Thr	Phe	Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr				
		515					520								